

Fig. 1

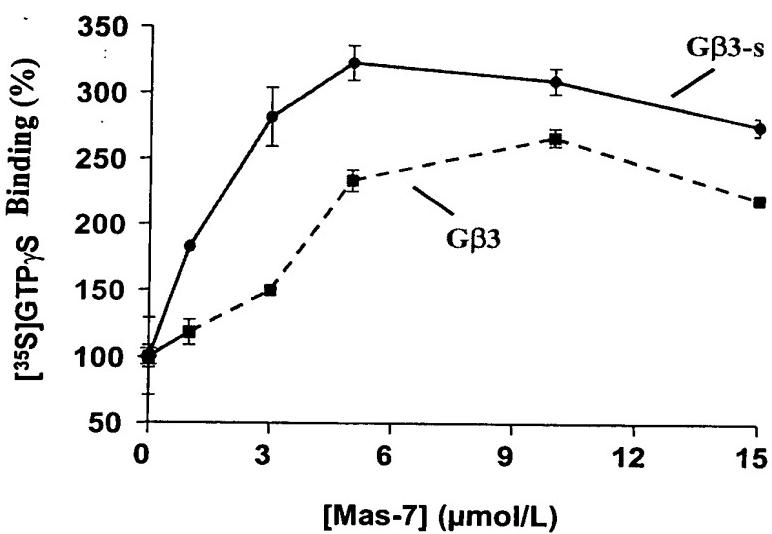


Fig. 2

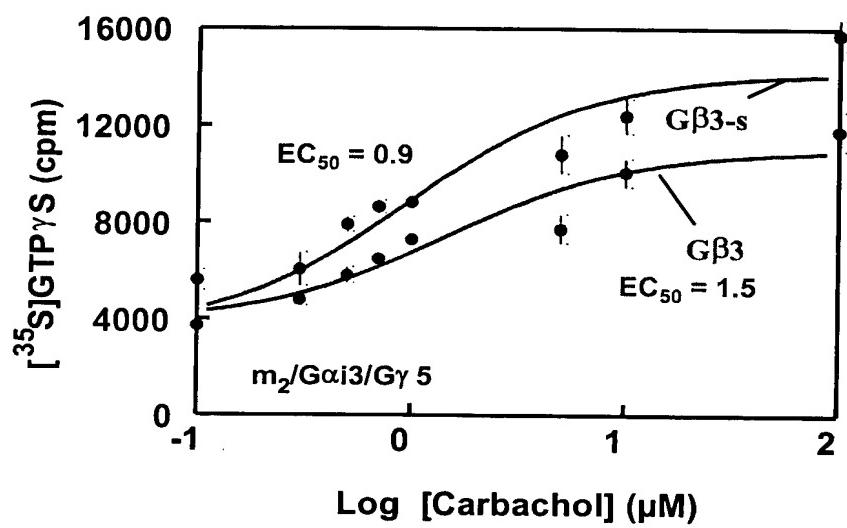


Fig. 3

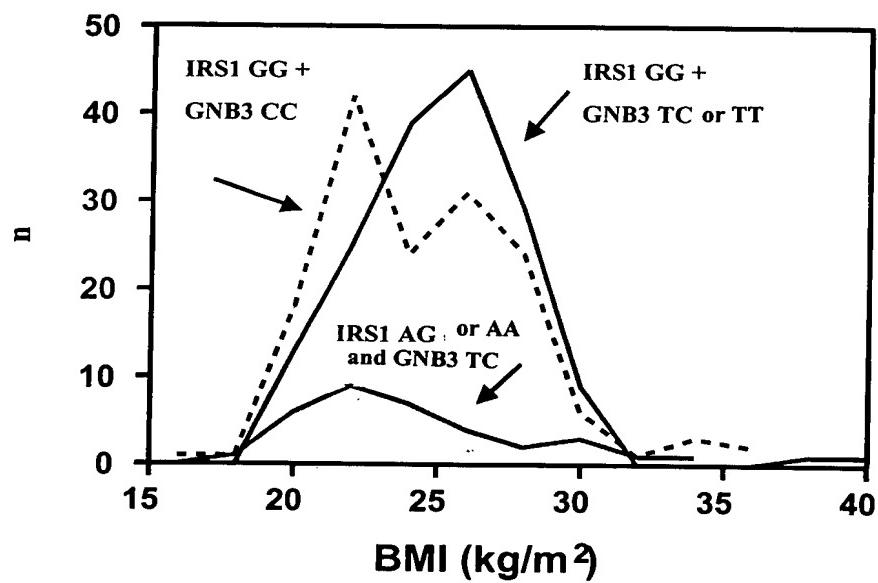


Fig. 4

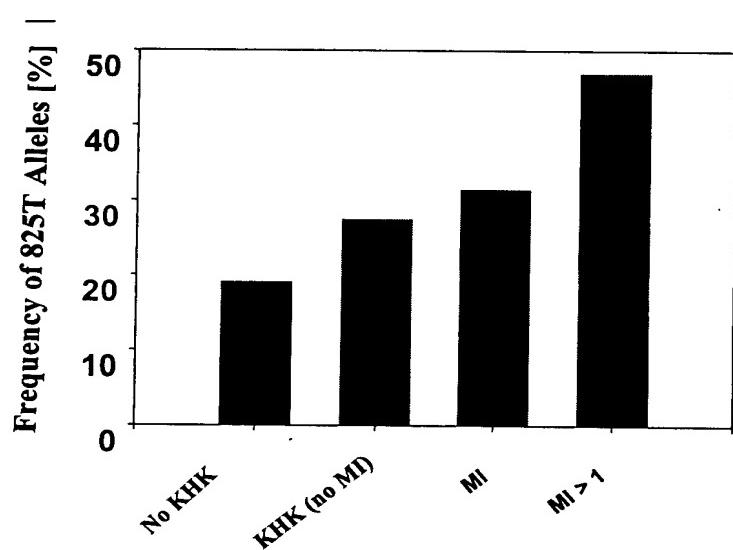


Fig. 5

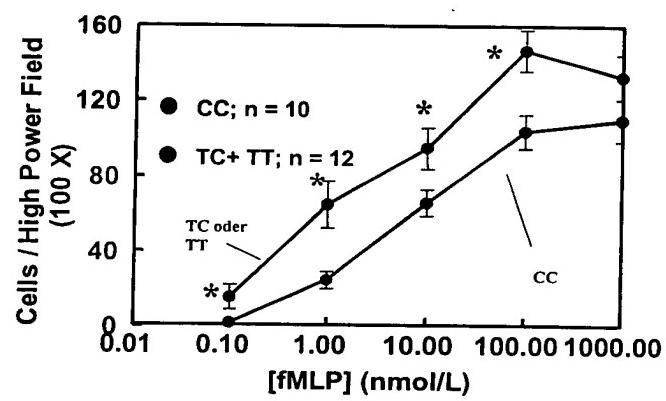


Fig. 6

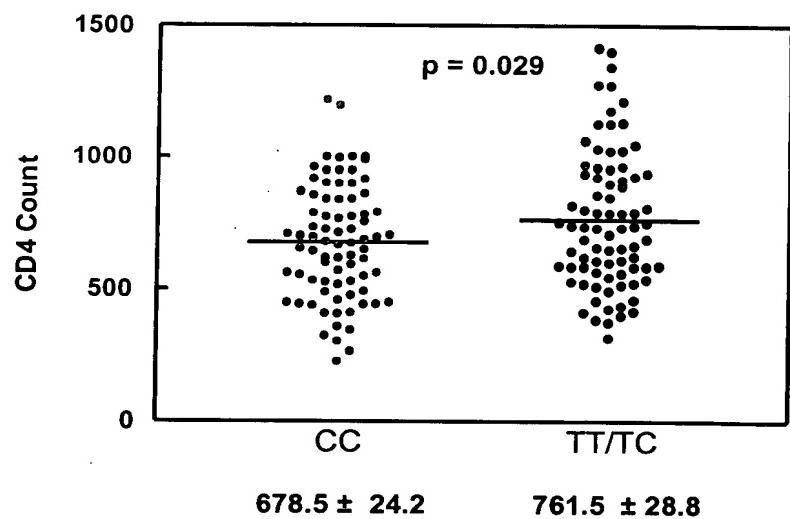


Fig. 7

### Enhanced Chemotaxis of T-Lymphocytes from 825T Allele Carriers

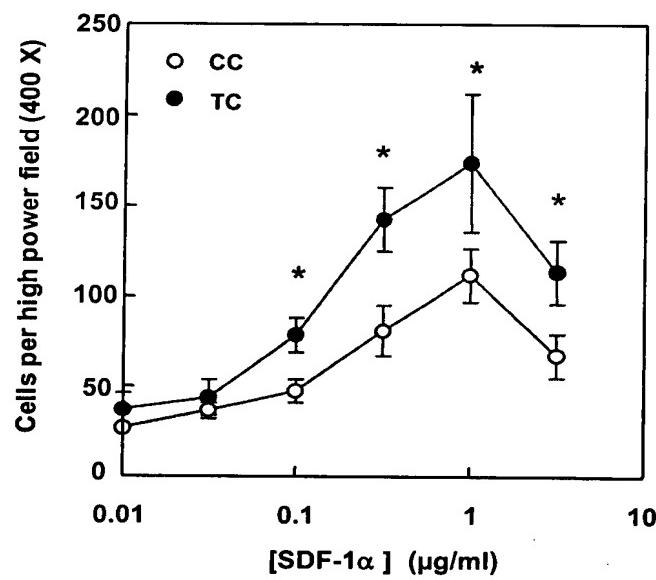


Fig. 8

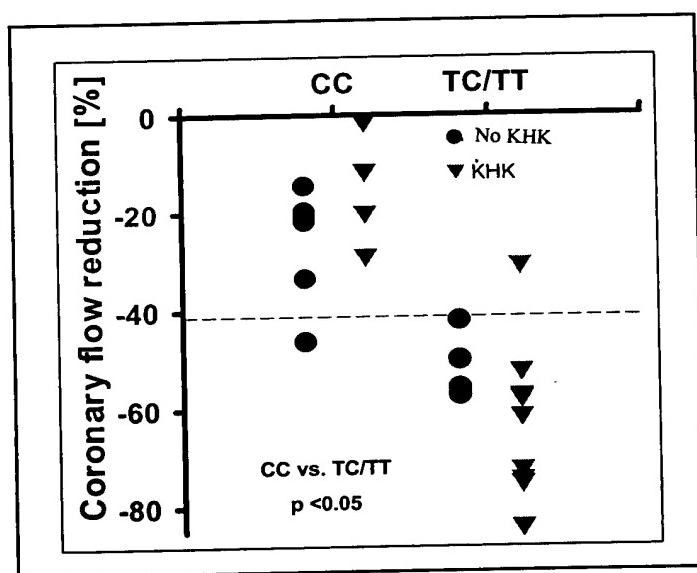
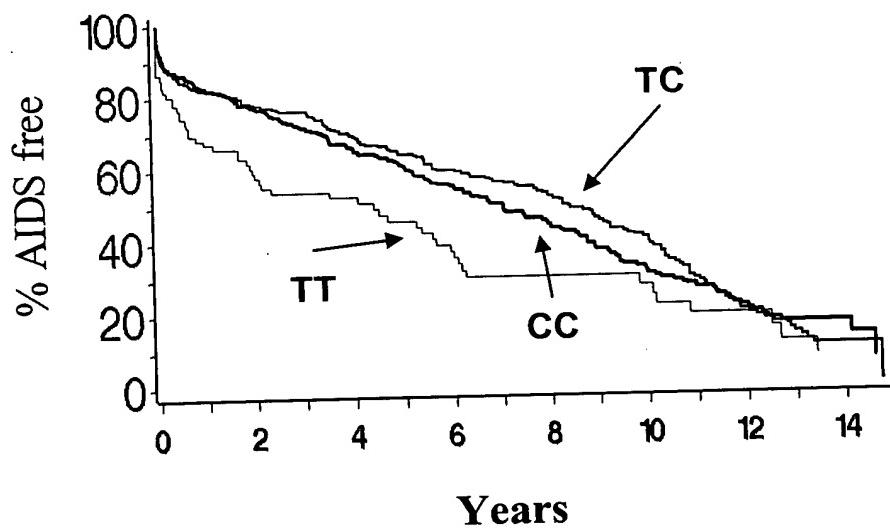


Fig. 9

### Time to AIDS

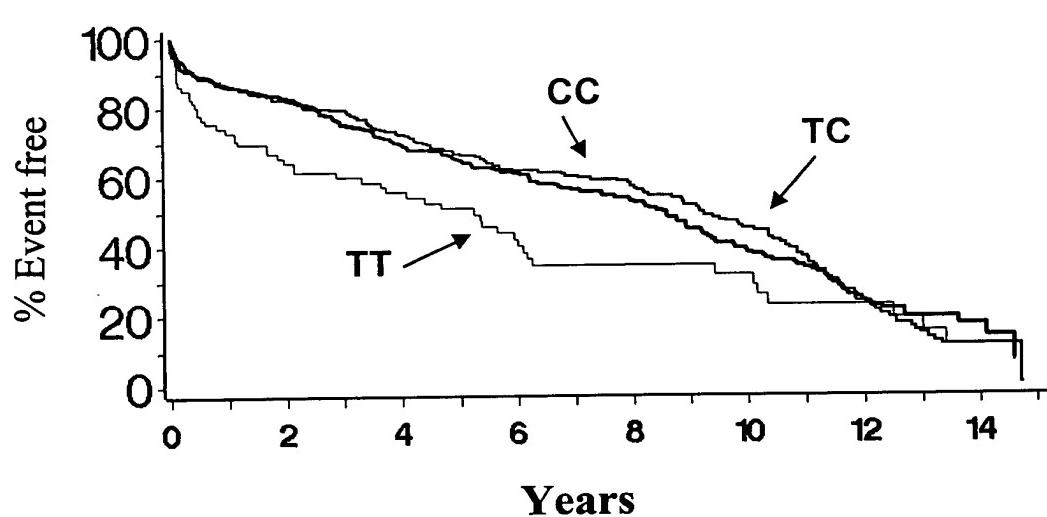
AIDS is defined as AIDS-defining disorders or CD4 count < 200



10/20

Fig. 10

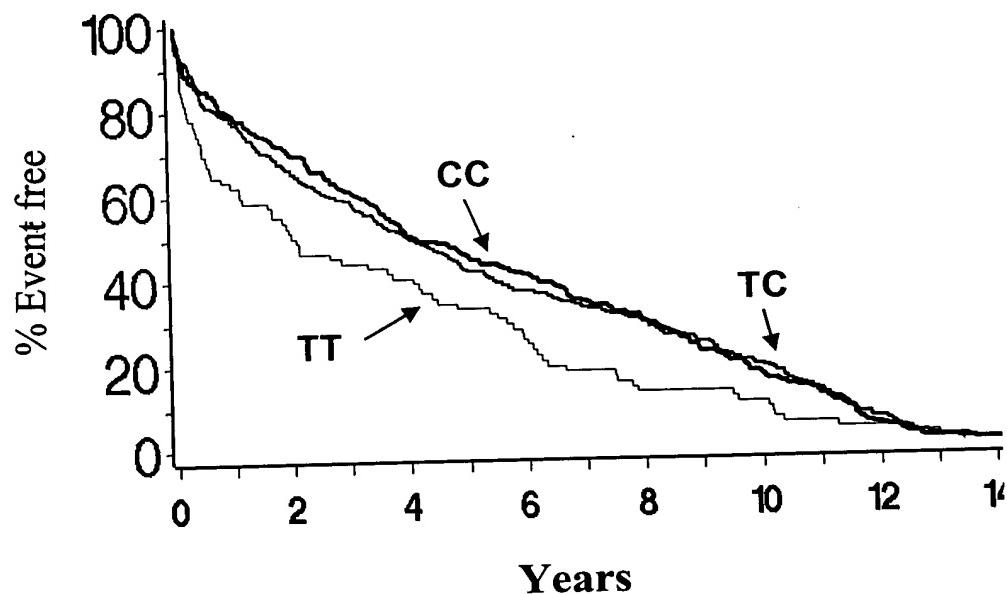
**Event: CD4 Cell Count Below 200 per  $\mu$ l**



11/20

Fig. 11

**Event: Lowest CD4 Cell Count**



12/20

Fig. 12

**Event: Time to maximum HIV Virus Load**  
Virus Copy Number determined by Quantitative PCR

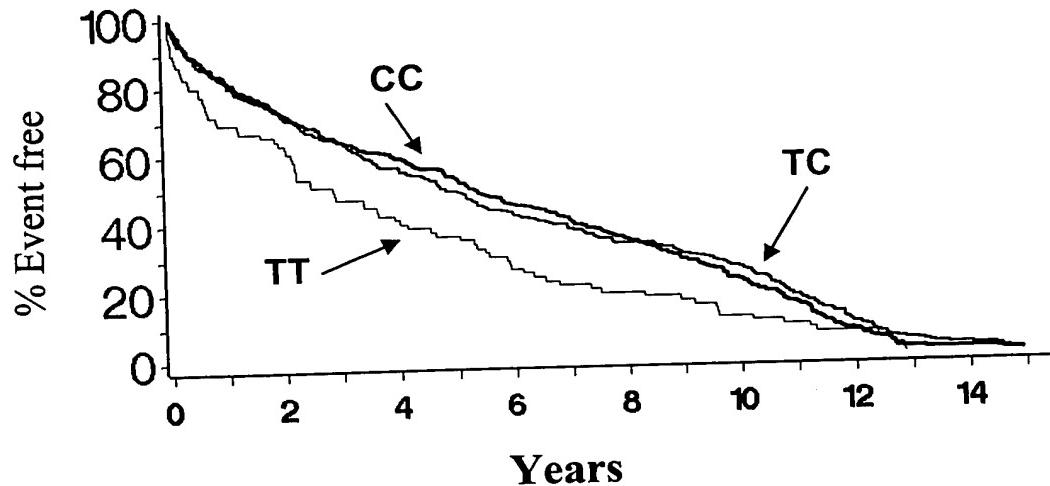
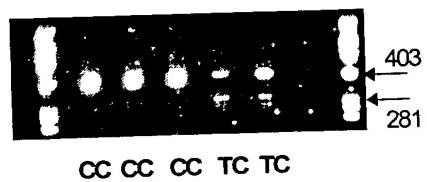


Fig. 13



13/20  
13/20  
13/20  
13/20  
13/20  
13/20

Fig. 14

### Potential Structures of G $\beta$ 3 and G $\beta$ 3s / G $\beta$ 3s-2

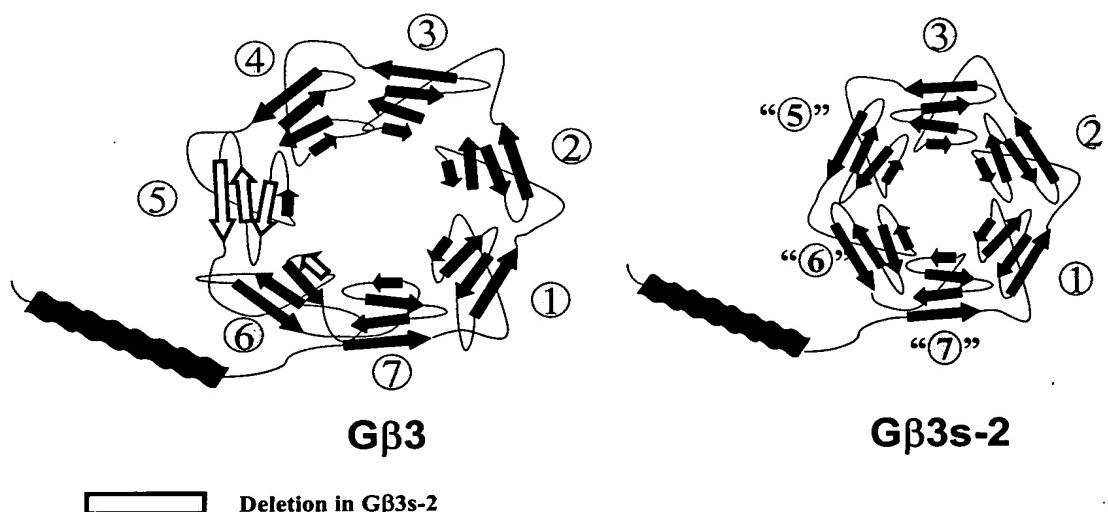


Fig. 15

1 Sf9 Cells  
varianten

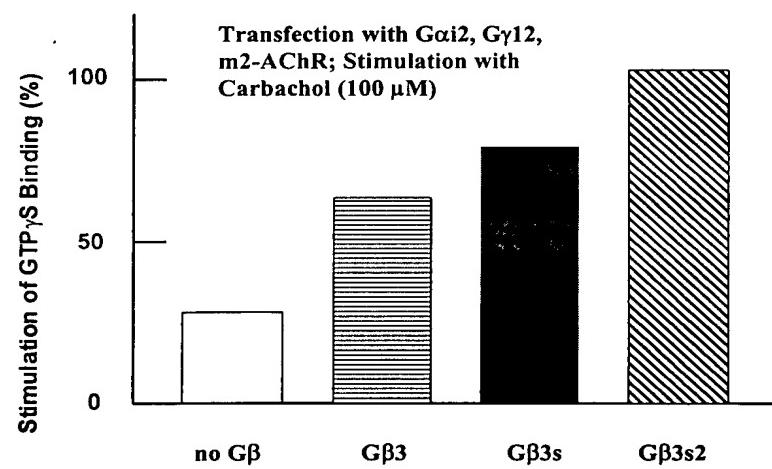


Fig. 16

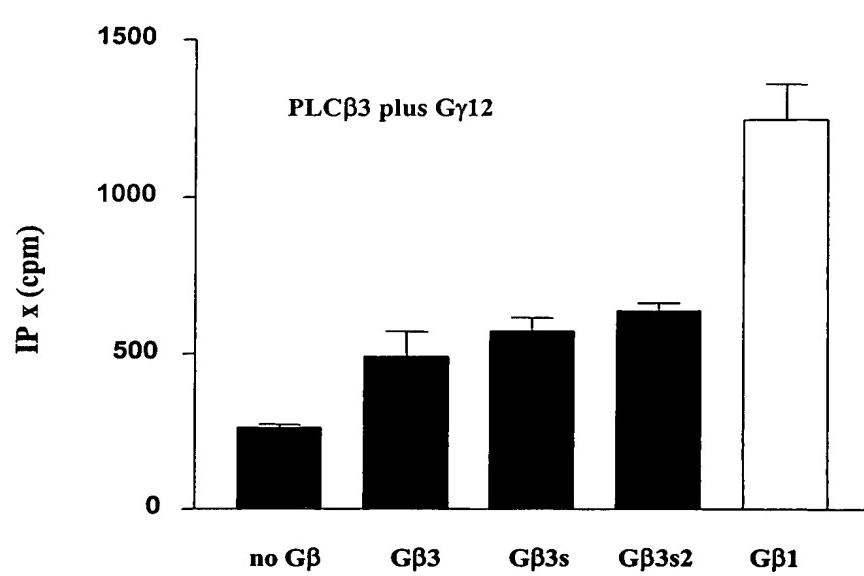


FIG. 17  $\beta$ 3-original sequence of Levine. The exons are underlined alternately. The area which is omitted by cryptic splice is bold-faced.

1 gggtcgATGG GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTAA GAAGCAGATT  
Start-ATG EXON 3 after Ansari-Lari  
Nucleotide 1-6 seem not to be affected

61 GCAGATGCCA GGAAAGCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGT TGGCCTAGAG /Beginning EXON 4 /EXON 5 Beginning ==> ENDE 1 KLON ANSARI

121 GTGGTGGAC GAGTCCAGAT GCGGACGCGG CGGACGTTAA GGGGACACCT GGCCAAGATT  
EXON 5

181 TACGCCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG  
EXON 5 / Beginning EXON 6

241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCAC GCGCTCCTCC / EXON 7

301 TGGGTCATGA CCTGTGCCTA TGCCCCATCA GGGAACTTTG TGGCATGTGG GGGGCTGGAC  
EXON 7

361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCCGGAG  
EXON 7

421 CTTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG  
EXON 7 /EXON 8

481 ACCAGCTCGG GGGACACCAC GTGTGCCTG TGGGACATTG AGACTGGGCA GCAGAACAGT  
EXON 8 /EXON 9

541 GTATTTGTGG GACACACGGG TGACTGCATG AGCCTGGCTG TGTCTCCTGA CTTCAATCTC  
EXON 9

cryptic SPLICING

541 GTATTTGTGG GACACACGGG TGACTGCATG AGCCTGGCTG TGTCTCCTGA CTTCAATCTC  
EXON 9

cryptic SPLICING

601 TTCATTCGG GGGCCTGTGA TGCCAGTGCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGC  
EXON 9

cryptic SPLICING /

661 CGTCAGACTT TCACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTTCTT CCCCAATGGA  
EXON 9 / Beginning EXON 10

721 GAGGCCATCT GCACGGGCTC GGATGACGCT TCCTGCCGCT TGTTTGACCT GCGGGCAGAC  
EXON 10

781 CAGGAGCTGA TCTGCTTCTC CCACGAGAGC ATCATCTGCG GCATCACGTC CGTGGCCTTC  
EXON 10 Polymorphism site acgtc tgt

841 TCCCTCAGTG GCCGCCTACT ATTGCTGGC TACGACGACT TCAACTGCCTA TGTCTGGAC  
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGCCACG ATAACAGGGT GAGCTGCCCTG  
EXON 10 /Beginning EXON 11

961 GGAGTCACAG CTGACGGGAT GGCTGTGCC ACAGGTTCTT GGGACAGCTT CCTCAAAATC  
EXON 11

1021 TGGAACTGAg gaggctggag aaaggaaagt ggaaggcagt qaacacactc agcagcccc  
EXON 11

End of Open Reading Frame

1081 tgcccgaccc catctcattc aggtgttctc ttctatattc cgggtgccat tcccactaag  
EXON 11

1141 ctttctctt tgagggcagt ggggagcatg ggactgtgcc ttggggaggc agcatcaggg  
EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccc aagtcctcac  
EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agccctttgc aggcccagca  
EXON 11

1321 gacttgagtc tgaggccccca ggccttagga ttccctcccccc agagccacta cctttgtcca  
EXON 11

1381 ggcctgggtg gtatagggcg tttggccctg tgactatggc tctggcacca cttaggtcct  
EXON 11

1441 ggcccttttc ttattcatgc ttctctttt ttctaccttt ttttctctcc taagacacct  
EXON 11

1501 gcaataaaagt gtagcacccct ggt  
EXON 11 POLY A SITE

Fig. 18 Sequence with two polymorphisms (Numbering after the Levine sequence)

gggtcgatgg	gggagatgga	gcaactgcgt	caggaagcgg	agcagctaa	gaagcagatt	60
gcagatgcca	gaaaagcctg	tgctgacgtt	actctggcag	agctgggtgc	tggcctagag	120
gtggtgggac	gagtccagat	gcggacgcgg	cgacgttaa	ggggacacct	ggccaagatt	180
tacgccatgc	actgggcccac	tgattctaag	ctgctggtaa	gtgcctcgca	agatggaaag	240
ctgatcgtgt	gggacagcta	caccaccaac	aagggcacg	ccatcccact	gcgcctcc	300
tgggtcatga	cctgtgccta	tgccccatca	gggaactttg	tggcatgtgg	ggggctggac	360
aacatgtgtt	ccatctacaa	cctcaaatacc	cgtgagggca	atgtcaaggt	cagccggag	420
ctttctgctc	acacaggta	tctctccctgc	tgccgcttcc	tggatgacaa	aatattgtg	480
accagctcgg	gggacaccac	gtgtgccttgc	tggacatttgc	agactggca	gcagaagact	540
gtatttgtgg	gacacacggg	tgactgeatg	agcctggctg	tgtctccatgc	cttcaatctc	600
ttcatttcgg	gggcctgtga	tgccagtgcc	aagctctggg	atgtgcgaga	ggggacctgc	660
cgtcagactt	tcactggcca	cgagtcggac	atcaacgcac	tctgttttctt	ccccaaatgg	720
gaggccatct	gcacgggctc	ggatgacgct	tccctggcgt	tgtttgaccc	gcgggcagac	780
caggagctga	tctgttttctc	ccacgagagc	atcatctgcg	gcacacgttc	tgtggccttc	840
tccctcagtg	gccgcctact	attcgctggc	tacgacgact	tcaactgca	tgtctggac	900
tccatgaagt	ctgagcgtgt	gggcattcc	tctggccacg	ataacaggg	gagctgcctg	960
ggagtccacag	ctgacgggat	ggctgtggcc	acaggttcc	gggacagctt	cctccaaatcc	1020
tggaactgag	gaggctggag	aaaggaaagt	ggaaggcagt	gaacacactc	agcagcccc	1080
tgcccgcaccc	catctcattc	agggtttctc	ttctatattc	cgggtgcac	tcccactaag	1140
ctttctccctt	tgagggcagt	ggggagcatg	ggactgtgc	tttgggaggc	agcatcaggg	1200
acacaggggc	aaagaactgc	cccatctcc	ccatggcct	tccctcccc	cagtccctcac	1260
agcctctccc	ttaatgagca	aggacaacct	gccctcccc	agcccttgc	aggcccagca	1320
gacttgagtc	tgaggccccca	ggcccttagga	ttccctcccc	agagccacta	cctttgtcca	1380
tctggcacta	ctaggcctgg	gtggtatagg	gcgtttggcc	ctgtgactat	ggctctggca	1440
ccacttagggt	cctggccctc	ttcttatca	tgctttctcc	tttttctacc	ttttttctc	1500
tcctaagaca	cctgcaataa	agtgtagcac	cctgg			1536

Fig. 19 Nucleic acid sequence of cDNA of G $\beta$ 3 and description of the deletion in G $\beta$ 3 and G $\beta$ 3s-2. Numbering referenced to the cDNA of Levine et al.(Levine, M.A., Smallwood, P.M., Moen, P.T., Jr., Helman, L.J., and Ahn, T.G. Molecular cloning of  $\beta$ 3 subunit, a third form of the G protein beta-subunit polypeptide.

*Proc.Natl.Acad.Sci.USA* 87(6):2329-2333, 1990) Here numbering does not begin with start codon ATG, but 6 nucleotides earlier in the 5' area.

```

1      gggtcgATGG GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTCAA GAAGCAGATT
Start-ATG   EXON 3
Nucleotide 1-6 seem not to be affected

61      GCAGATGCCA GGAAAGCCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGTC TGGCCTAGAG
/Beginn EXON 4                               /EXON 5 Beginning

121     GTGGTGGGAC GAGTCCAGAT GCGGACGCGG CGGACGTTAA GGGGACACCT GGCCAAGATT
EXON 5

181     TACGCCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG
EXON 5                               / Beginning EXON 6

241     CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCACT GCGCTCCTCC
EXON 6                               / EXON 7

301     TGGGTCATGA CCTGTGCCTA TGCCCCATCA GGGAACTTTG TGGCATGTGG GGGGCTGGAC
EXON 7

361     AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCCGGAG
EXON 7

421     CTTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG
EXON 7                               /EXON 8

```

**Deletion bei C<sub>8</sub>C<sub>9</sub>**

481 ACCAGCTCGG GGGACACCAC GTGTCCTTTC TGGGACANTC AGACATGGCA CCACACAC  
EXON 8 / EXON 9

541 GTAAATTCCTGC GACAGACCC TCACCTGATC ACCGACCCCTC TCTCTCTCA CTTGCTAC  
EXON 9

581 TTCATTTTCCC CCCCTTCTCTC TCCCTTGCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGC  
EXON 9

**Deletion bei C<sub>8</sub>C<sub>9</sub>**

661 CGTCAGACTT TCACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTCT CCCAAATGCA  
EXON 9 / Beginn EXON 10  
Intron dazwischen 1607 bp

**Deletion in G<sub>B3s2</sub>**

721 GAGGCCATCTGGCACGGGCTC GGATGACGCT TCCTGCCGCT TGTTTGACCT GCGGGCAGAC  
EXON 10

781 CAGCACCTGA TCTGGCTCTC CCACGGAGACC ATCATCTCCG GATGACGCTC AGTCCCTTCTC  
EXON 10 polymorphism site acgtc tgt

841 TCCCTCAGTG GCCGCCTACT ATTGCTGGC TACGACGACT TCAACTGCAA TGTCTGGAC  
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGGCCACG ATAACAGGGT GAGCTGCCTG  
EXON 10 /Beginning EXON 11 (Intron dazw. 989 bp)

961 GGAGTCACAG CTGACGGAT GGCTGTGGCC ACAGGTT CCTCAAAATC  
EXON 11

1021 TGGAACGTGAg gaggctggag aaagggaaagt ggaaggcagt gaacacactc agcagcccc  
EXON 11  
End of Open Reading Frame B3-3

1081 tgcccgaccc catctcatTC aggtttctc ttctatattc cgggtgccat tcccactaag  
EXON 11

1141 ctttctcctt tgagggcagt ggggagcatg ggactgtgcc tttgggaggc agcatcaggg  
EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccc aagtcctcac  
EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agccctttgc aggcccagca  
EXON 11

1321 gacttgagtc tgaggccccca ggcccttagga ttccctcccc agagccacta cctttgtcca  
EXON 11

1381 ggcctgggtg gtataggcg tttggccctg tgactatggc tctggcacca ctagggtcct  
EXON 11

1441 ggccctcttc ttattcatgc tttctcctt ttctacctt tttctctcc taagacacct  
EXON 11

1501 gcaataaaagt gtagcaccct ggt  
EXON 11      POLY A SITE

FIG. 20 Amino acid sequence of G $\beta$ 3s-2 (Combined production)

atg ggg gag atg gag caa ctg cgt cag gaa gcg gag cag ctc aag aag	48		
Met Gly Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu Lys Lys			
5	10	15	
cag att gca gat gcc agg aaa gcc tgt gct gac gtt act ctg gca gag	96		
Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu Ala Glu			
20	25	30	
ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg acg cgg	144		
Leu Val Ser Gly Leu Val Val Gly Arg Val Gln Met Arg Thr Arg			
35	40	45	
cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac tgg gcc	192		
Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala			
50	55	60	
act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag ctg atc	240		
Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile			
65	70	75	75
gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca ctg cgc	288		
Val Trp Asp Ser Tyr Thr Asn Lys Val His Ala Ile Pro Leu Arg			
80	85	90	
tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac ttt gtg	336		
Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val			
95	100	105	
gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc aaa tcc	384		
Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser			
110	115	120	
cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac aca ggt	432		
Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly			
125	130	135	
tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg acc agc	480		
Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser			
140	145	150	155
tcg ggg gac acc acg tgt gcc ttg tgg gac att gag act ggg cag cag	528		
Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln			
160	165	170	175
aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctc gct gtg	576		
Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val			
180	185	190	
tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc agt gcc	624		
ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala			
195	200	205	

aag ctc tgg gat gtg cga gag ggg acc tgc cgt cag act ttc act ggc 672  
Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly  
210 215 220

cag gag tcg gac atc aac gcc atc tgt ttc ttc tcc ctc agt ggc cgc 720  
His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Ser Leu Ser Gly Arg  
225 230 235

cta cta ttc gct ggc tac gac gac ttc aac tgc aat gtc tgg gac tcc 768  
Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser  
240 245 250 255

atg aag tct gag cgt gtg ggc atc ctc tct ggc cac gat aac agg gtg 816  
Met Lys Ser Glu Arg Val Gly Ile Leu Ser Gly His Asp Asn Arg Val  
260 265 270

agc tgc ctg gga gtc aca gct gac ggg atg gct gtg gcc aca ggt tcc 864  
Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser  
275 280 285

tgg gac agc ttc ctc aaa atc tgg aac tga 894  
Trp Asp Ser Phe Leu Lys Ile Trp Asn \*\*\*  
290 295